Shown is the 3'UTR of the human IL1B sequence from accession number M15330.
* Represents the stop codon.

*AGAGAGCTGTACCCAGAGAGTCCTGTGCTGAATGTGGACTCAATCCCTAG
GGCTGGCAGAAAGGGAACAGAAAGGTTTTTGAGTACGGCTATAGCCTGGAC
TTTCCTGTTGTCTACACCAATGCCCAACTGCCTGCCTTAGGGTAGTGCTAA
GAGGATCTCCTGTCCATCAGCCAGGACAGTCAGCTCTCTCCTTTCAGGGCC
AATCCCCAGCCCTTTTGTTGAGCCAGGCCTCTCTCACCTCTCCTACTCACT
TAAAGCCCGCCTGACAGAAACCACGGCCACATTTGGTTCTAAGAAACCCTC
TGTCATTCGCTCCCCACATTCTGATGAGCAACCGCTTCCCT***ATTTATTTATTT***
TATTTGTTTGTTTATTCATTGGTCTA***ATTTA***TTCAAAGGGGGCAAG
AAGTAGCAGTGTCTGTAAAAGAGCCTAGTTTTTAATAGCTATGGAATCAAT
TCAATTTGGACTGGTGTGCTCTCTTTAAATCAAGTCCTTTAATTAAGACTG
AAAATATATAAGCTCAGATT***ATTTA***AATGGGAAT***ATTTA***TAAATGAGCAAA
TATCATACTGTTCAATGGTTCTGAAATAACTTCTCTGAAG

FIGURE 1

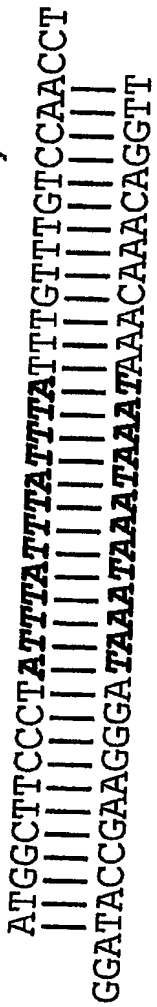
ATGGCTTCCCTATTTATTTATTTATTTGTTTGTCCAACCT
GGATACCGAAGGGATAAATAAATAAATAAACAAACAGGTT

FIGURE 2

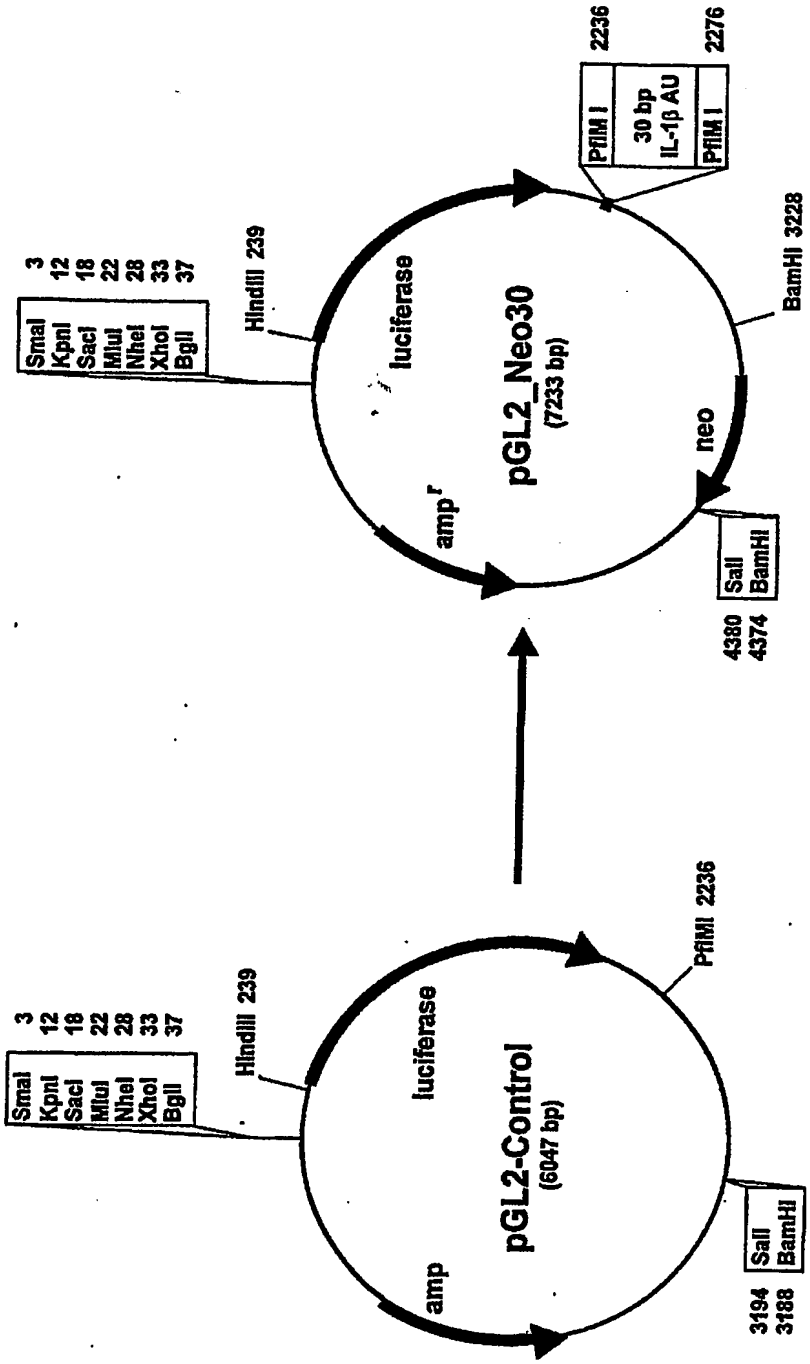
pGL2-Control
(6047 bp)
luciferase
amp
Hindlll 239
PflMI 2236
3 12 18 22 28 33 37
SmaI KpnI SacI MluI NheI XhoI BglII
SalI BamHI
3194 3188
pGL2_Neo30
(7233 bp)
luciferase
amp
neo
Hindlll 239
2236
2276
PflM I
30 bp IL-1β AU
PflM I
BamHI 3228
SalI BamHI
4380 4374

FIGURE 3A

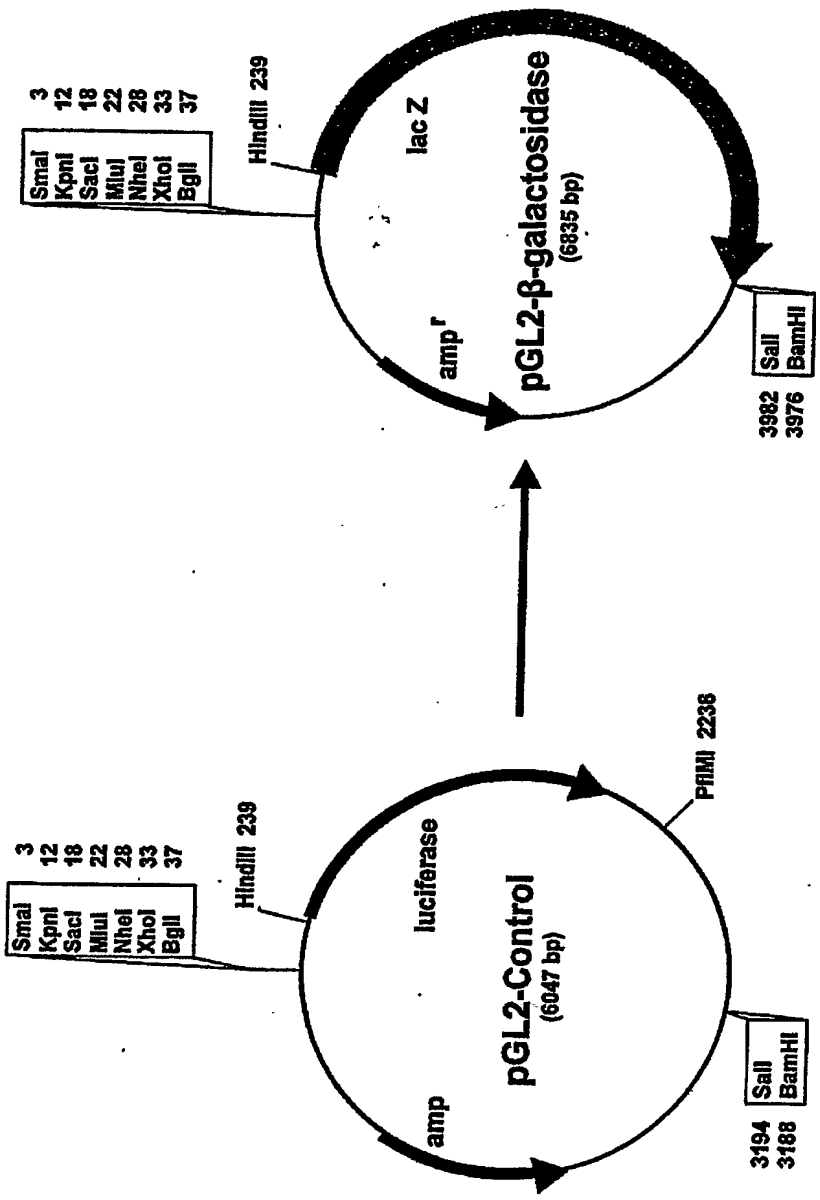
pGL2-β-galactosidase
(6835 bp)
lac Z
amp^r
HindIII 239
SmaI KpnI SacI MluI NheI XhoI BglII
3 12 18 22 28 33 37
SalI BamHI
3982 3976
pGL2-Control
(6047 bp)
luciferase
amp
HindIII 239
SmaI KpnI SacI MluI NheI XhoI BglII
3 12 18 22 28 33 37
PflMI 2236
SalI BamHI
3194 3188

FIGURE 3 B

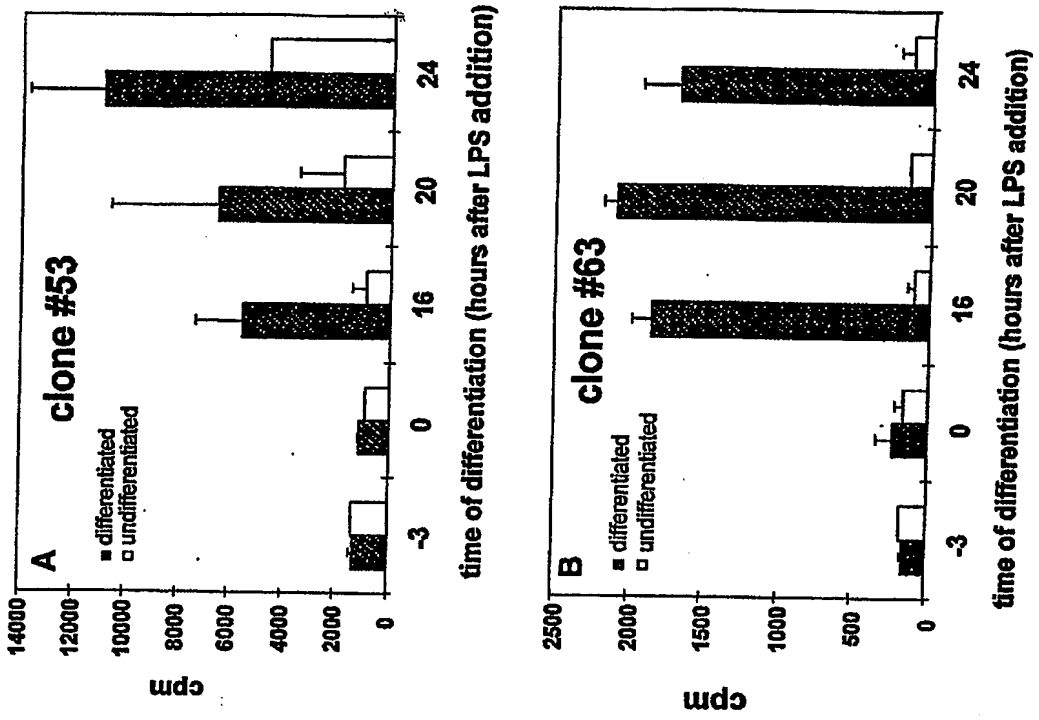
A
clone #53
differentiated
undifferentiated
cpm
14000
12000
10000
8000
6000
4000
2000
0
-3
0
16
20
24
time of differentiation (hours after LPS addition)
B
clone #63
differentiated
undifferentiated
cpm
2500
2000
1500
1000
500
0
-3
0
16
20
24
time of differentiation (hours after LPS addition)

FIGURE 4

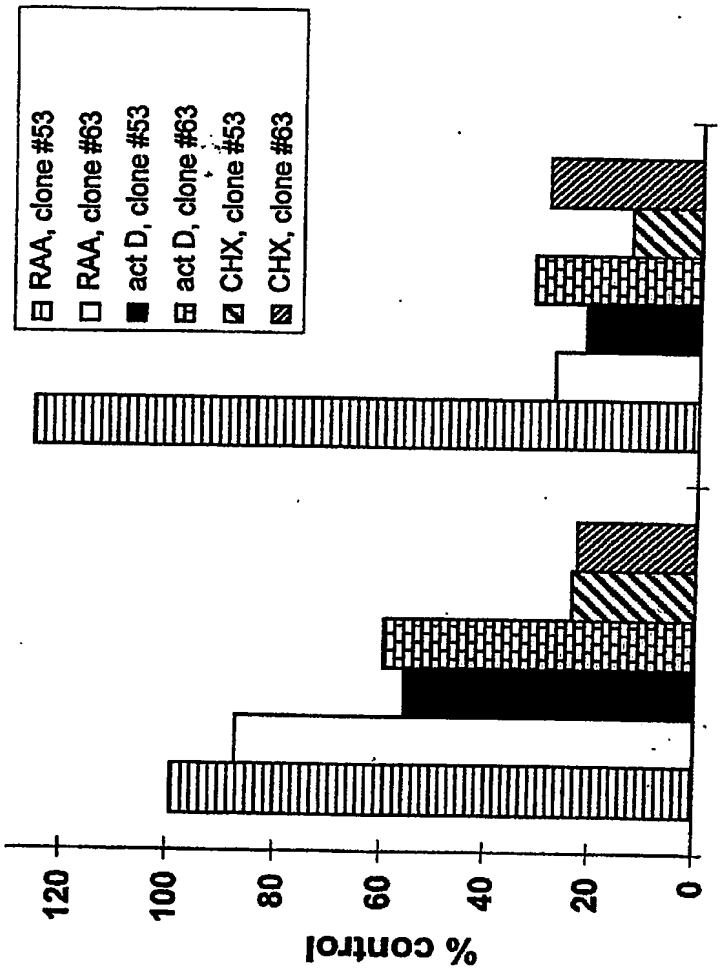
RAA, clone #53
RAA, clone #63
act D, clone #53
act D, clone #63
CHX, clone #53
CHX, clone #63
% control
120
100
80
60
40
20
0
4
8
hours after addition of compounds

FIGURE 5

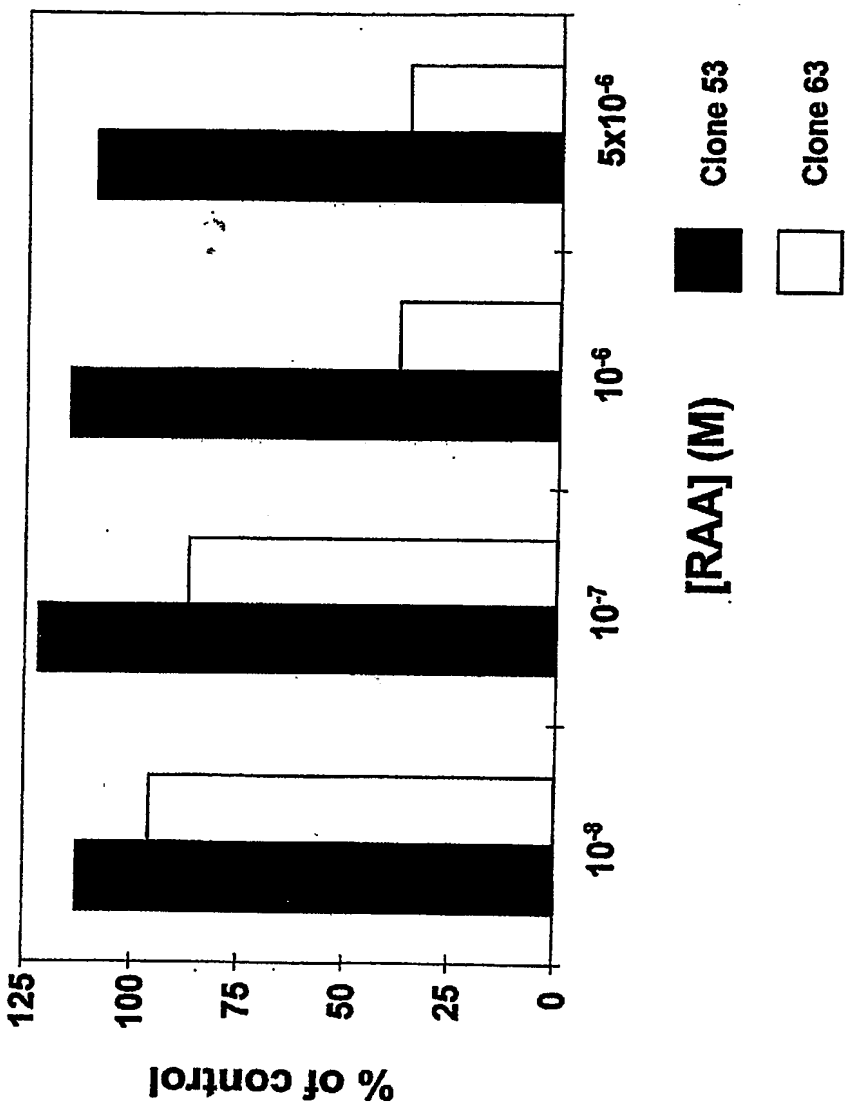
% of control
125
100
75
50
25
0
10-8
10-7
10-6
5x10-6
[RAA] (M)
Clone 53
Clone 63

FIGURE 6

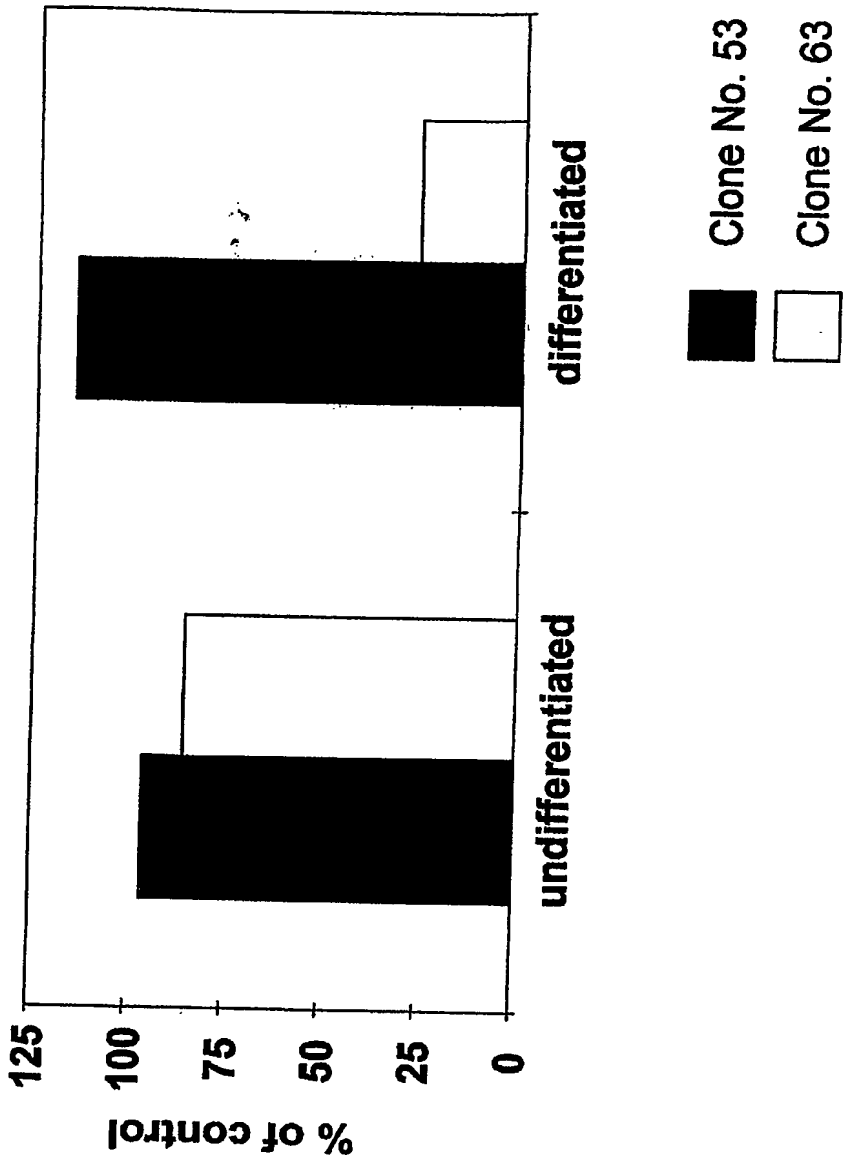
Clone No. 53
Clone No. 63
differentiated
undifferentiated
% of control
125
100
75
50
25
0

FIGURE 7

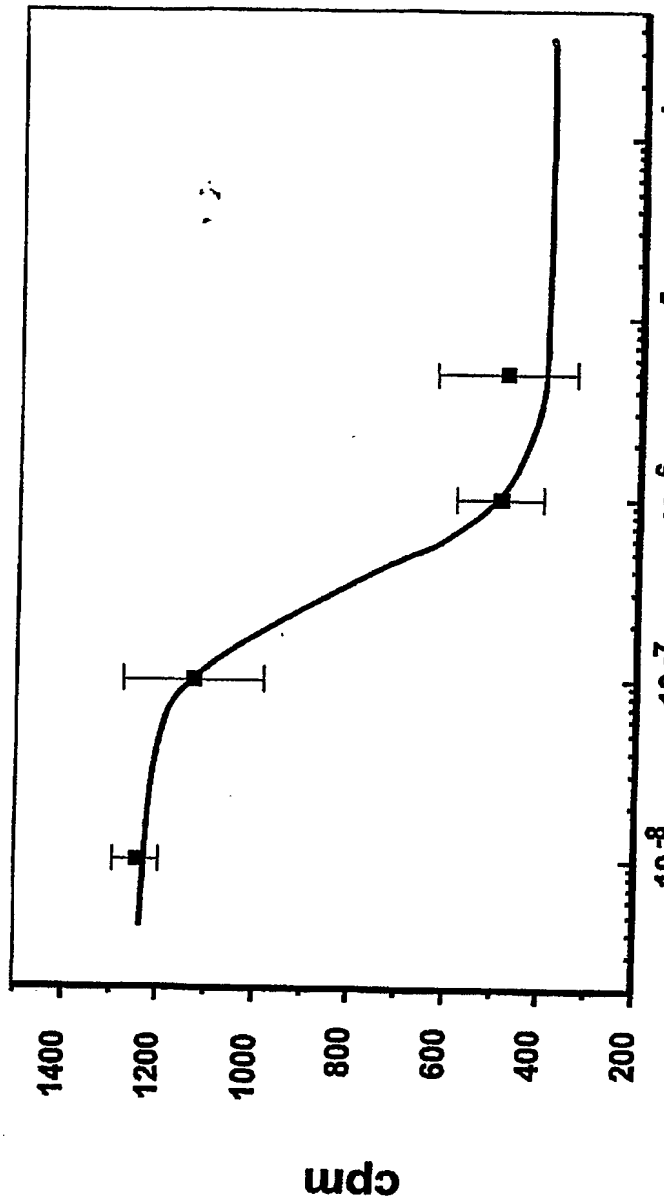

FIGURE 8

NotI

1 GCGGCCGCCA CAGCAGCCTC TGAAGTTGGA CAGCAAAACC ATTGCTTCAC TACCCATCGG TGTCCATTTA TAGAATAATG TGGGAAGAAA CAAACCCGTT

101 TTATGATTTA CTCATTATCG CCTTTTGACA GCTGTGCTGT AACACAAGTA GATGCCTGAA CTTGAATTAA TCCACACATC AGTAATGTAT TCTATCTCTC

201 TTTACATTTT GGTCTCTATA CTACATTATT AATGGGTTTT GTGTACTGTA AAGAATTTAG CTGTATCAAA CTAGTGCATG AATAGATTCT CTCCTGATTA

301 TTTATCACAT AGCCCCTTAG CCAGTTGTAT ATTATTCTTG TGGTTTGTGA CCCAATTAAG TCCTACTTTA CATATGCTTT AAGAATCGAT GGGGGATGCT

401 TCATGTGAAC GTGGCAGTTC AGCTGCTTCT CTTGCCTAAG TATTCCTTTC CTGATCACTA TGCATTTTAA AGTTAAACAT TTTTAAGTAT TTCAGATGCT

501 TTAGAGAGAT TTTTTTTTCC ATGACTGCAT TTTACTGTAC AGATTGCTGC TTCTGCTATA TTTGTGATAT AGGAATTAAG AGGATACACA CGTTTGTTTC

601 TTCGTGCCTG TTTTATGTGC ACACATTAGG CATTGAGACT TCAAGCTTTT CTTTTTTTGT CCACGTATCT TTGGGTCTTT GATAAAGAAA AGAATCCCTG

701 TTCATTGTAA GCACTTTTAC GGGGCGGGTG GGGAGGGGTG CTCTGCTGGT CTTCAATTAC CAAGAATTCT CCAAAACAAT TTTCTGCAGG ATGATTGTAC

801 AGAATCATTG CTTATGACAT GATCGCTTTC TACACTGTAT TACATAAATA AATTAAATAA AATAACCCCG GGCAAGACTT TTCTTTGAAG GATGACTACA

901 GACATTAAAT AATCGAAGTA ATTTTGGGTG GGGAGAAGAG GCAGATTCAA TTTTCTTTAA CCAGTCTGAA GTTTCATTTA TGATACAAAA GAAGATGAAA

1001 ATGGAAGTGG CAATATAAGG GGATGAGGAA GGCATGCCTG GACAAACCCT TCTTTTAAGA TGTGTCTTCA ATTTGTATAA AATGGTGTTT TCATGTAGCG

1101 GCCGC
NotI

Length: 1105 bp

FIGURE 9

NotI

1 GCGGCCGCTG AAGTCAACAT GCCTGCCCCA AACAAATATG CAAAAGGTTC ACTAAAGCAG TAGAAATAAT ATGCATTGTC AGTGATGTAC CATGAAACAA

101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA CAGACAGACA CACACACACA CAACAATTAA CAGTCTTCAG GCAAAACGTC

201 GAATCAGCTA TTTACTGCCA AAGGGAAATA TCATTTATTT TTTACATTAT TAAGAAAAAA AGATTTATTT ATTTAAGACA GTCCCATCAA AACTCCTGTC

301 TTTGGAAATC CGACCACTAA TTGCCAAGCA CCGCTTCGTG TGGCTCCACC TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGCCG

401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGGTGT TCATTCACTT

501 GCATTTCTTT GCCCTGGGGG CTGTGATATT AACAGAGGGA GGGTTCCTGT GGGGGGAAGT CCATGCCTCC CTGGCCTGAA GAAGAGACTC TTTGCATATG

601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATGGGAAAA

701 ATGCCCTTAA ATCATAGGAA AGTATTTTTT TAAGCTACCA ATTGTGCCGA GAAAAGCATT TTAGCAATTT ATACAATATC ATCCAGTACC TTAAGCCCTG

801 ATTGTGTATA TTCATATATT TTGGATACGC ACCCCCCAAC TCCCAATACT GGCTCTGTCT GAGTAAGAAA CAGAATCCTC TGGAACTTGA GGAAGTGCGG

901 CCGC

NotI

FIGURE 10

Length: 904 bp

stop codon {Bold/Italics/Underline}
bcl-2α-short construct:
AUUUA {Bold/Underline}
Restriction Sites {Bold}
NotI
1 GCGGCCGCTG AAGTCAACAT GCCTGCCCCA AACAAATATG CAAAGGTTC
51 ACTAAAGCAG TAGAAATAAT ATGCATTGTC AGTGATGTAC CATGAAACAA
101 AGCTGCAGGC TGTTTAAGAA AAAATAACAC ACATATAAAC ATCACACACA
151 CAGACAGACA CACACACACA CAACAATTAA CAGTCTTCAG GCAAAACGTC
201 GAATCAGCTA TTTACTGCCA AAGGAAATA TCATTTATTT TTTACATTAT
251 TAAGAAAAAA AGATTTATTT ATTTAGACA GTCCCATCAA AACTCCTGTC
301 TTTGGAAATC CGACCACTAA TTGCCAAGCA CCGCTTCGTG TGGCTCCACC
351 TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG
401 GATCACCATC TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG
451 AAGCTGGCTT TCTGGCTGCT GGAGGCTGGG GAGAAGGTGT TCATTCACTT
501 GCATTTCTTT GCCCTGGGGG CTGTGATATT AACAGAGGGA GGGTTCCTGT
551 GGGGGGAAGT CCATGCCTCC CTGGCCTGAA GAAGACACTC TTTGCATATG
601 ACTCACATGA TGCATACCTG GTGGGAGGAA AAGAGTTGGG AACTTCAGAT
651 GGACCTAGTA CCCACTGAGA TTTCCACGCC GAAGGACAGC GATGGGAAAA
701 ATGCGGCCGC
NotI
Length: 710 bp

FIGURE 11

stop codon {Bold/Italics/Underline}
c-myc construct:
CRD
AUUUA {Bold/Underline}
CRD:
potential polyA signal sequence {Bold/Italics}
coding region instability determinant {Underline}
Restriction Sites {Bold}
NotI
1 GCGGCCGCTC GGAGCTTTTT TGCCCTGCGT GACCAGATCC CGGAGTTGGA
51 AAACAATGAA AAGGCCCCCA AGGTAGTTAT CCTTAAAAAA GCCACAGCAT
101 ACATCCTGTC CGTCCAAGCA GAGGAGCAAA AGCTCATTTC TGAAGAGGAC
151 TTGTTGCGGA AACGACGAGA ACAGTTGAAA CACAAACTTG AACAGCTACG
201 GAACTCTTGT GCGTAAGGAA AAGTAAGGAA AACGATTCCT TCTGACAGAA
251 ATGTCCTGAG CAATCACCTA TGAACTTGTT TCAAATGCAT GATCAAATGC
301 AACCTCACAA CCTTGCCTGA GTCTTGAGAC TGAAAGATTT AGCCATAATG
351 TAAACTGCCT CAAATTGGAC TTTGGGCATA AAAGAACTTT TTTATGCTTA
401 CCATCTTTTT TTTTTCTTTA ACAGATTTGT ATTTAAGAAT TGTTTTTAAA
451 AAATTTTAAG ATTTACACAA TGTTTCTCTG TAAATATTGC CATTAAATGT
501 AAATAACTTT AATAAAACGT TTATAGCAGT TACACAGAAT TTCAATCCTA
551 GTATATAGTA CCTAGTATTA TAGGTACTAT AAACCCTAAT TTTTTTATTT
601 TAAGTACATT TTGCTTTTTA AAGTTGATTT TTTTCTATTG TTTTTAGAAA
651 AAATAAATA ACTGGCAAAT ATATCATTGA GCCATATG
NdeI
Length: 688 bp

FIGURE 12

stop codon {Bold/Italics/Underline}
TNF-α construct:
AUUUA {Bold/Underline}
Potential polyA signal sequence {Bold/Italics}
Restriction Sites {Bold}
NotI
1 GCGGCCGCTG AGGAGGACGA ACATCCAACC TTCCCAAACG CCTCCCCTGC CCCAATCCCT
61 TTATTACCCC CTCCTTCAGA CACCCTCAAC CTCTTCTGGC TCAAAAAGAG AATTGGGGGC
121 TTAGGGTCGG AACCCAAGCT TAGAACTTTA AGCAACAAGA CCACCACTTC GAAACCTGGG
181 ATTCAGGAAT GTGTGGCCTG CACAGTGAAG TGCTGGCAAC CACTAAGAAT TCAAACTGGG
241 GCCTCCAGAA CTCACTGGGG CCTACAGCTT TGATCCCTGA CATCTGGAAT CTGGAGACCA
301 GGGAGCCTTT GGTTCTGGCC AGAATGCTGC AGGACTTGAG AAGACCTCAC CTAGAAATTG
361 ACACAAGTGG ACCTTAGGCC TTCCTCTCTC CAGATGTTTC CAGACTTCCT TGAGACACGG
421 AGCCCAGCCC TCCCCATGGA GCCAGCTCCC TCATTTATG TTTGCACTTG TGATTATTTA
481 TTATTTATTT ATTATTTATT TATTTACAGA TGAATGTATT TATTTGGGAG ACCGGGTTAT
541 CCTGGGGGAC CCAATGTAGG AGCTGCCTTG GCTCAGACAT GTTTTCCGTG AAAACGGAGC
601 TGAACAATAG GCTGTTCCCA TGTAGCCCCC TGGCCTCTGT GCCTTCTTTT GATTATGTTT
661 TTTAAAATAT TTATCTGATT AAGTTGTCTA AACAATGCTG ATTTGGTGAC CAACTGTCAC
721 TCATTGCTGA GCCTCTGCTC CCCAGGGGAG TTGTGTCTGT AATCGCCCTA CTATTCAGTG
781 GCGAGAAATA AAGTTTGCTT CATATG
NdeI
Length: 806 bp

FIGURE 13

stop codon {Bold/Italics/Underline}
IL-18 construct:
AUUUA {Bold/Underline}
Potential polyA signal sequence {Bold/Italics}
Restriction Sites {Bold}
NotI
1 GCGGCCGCTA AAGAGAGCTG TACCCAGAGA GTCCTGTGCT GAATGTGGAC
51 TCAATCCCTA GGGCTGGCAG AAAGGAACA GAAAGGTTTT TGAGTACGGC
101 TATAGCCTGG ACTTTCCTGT TGTCTACACC AATGCCCAAC TGCCTGCCTT
151 AGGCTAGTGC TAAGAGGATC TCCTGTCCAT CAGCCAGGAC AGTCAGCTCT
201 CTCCTTTCAG GGCCAATCCC CAGCCCTTTT GTTGAGCCAG GCCTCTCTCA
251 CCTCTCCTAC TCACTTAAAG CCCGCCTGAC AGAAACCACG GCCACATTTG
301 GTTCTAAGAA ACCCTCTGTC ATTCGCTCCC ACATTCTGAT GAGCAACCGC
351 TTCCCTATTT ATTTATTTAT TTGTTTGTTT GTTTTATTCA TTGGTCTAAT
401 TTATTCAAAG GGGGCAAGAA GTAGCAGTGT CTGTAAAAGA GCCTAGTTTT
451 TAATAGCTAT GGAATCAATT CAATTTGGAC TGGTGTGCTC TCTTTAAATC
501 AAGTCCTTTA ATTAAGACTG AAAATATATA AGCTCAGATT ATTTAAATGG
551 GAATATTTAT AAATGAGCAA ATATCATACT GTTCAATGGT TCTGAAATAA
601 ACTTCACCAT ATG
NdeI
Length: 613 bp

FIGURE 14

NotI

1 GCGGCCGCAT TGCTGTGCTT TGGGGATTCC CTCCACATGC TGCACGCGCA TCTCGCCCCC AGGGGCACTG CCTGGAAGAT TCAGGAGCCT GGGCGGCCTT

101 CGCTTACTCT CACCTGCTTC TGAGTTGCCC AGGAGGCCAC TGGCAGATGT CCCGGCGAAG AGAAGAGACA CATTGTTGGA AGAAGCAGCC CATGACAGCT

201 CCCCTTCCTG GGACTCGCCC TCATCCTCTT CCTGCTCCCC TTCCTGGGGT GCAGCCTAAA AGGACCTATG TCCTCACACC ATTGAAACCA CTAGTTCTGT

301 CCCCCCAGGA GACCTGGTTG TGTGTGTGTG AGTGGTTGAC CTTCCTCCAT CCCCTGGTCC TTCCCTTCCC TTCCCGAGGC ACAGAGAGAC AGGGCAGGAT

401 CCACGTGCCC ATTGTGGAGG CAGAGAAAAG AGAAAGTGTT TTATATACGG TACTTATTTA ATATCCCTTT TTAATTAGAA ATTAAAACAG TTAATTTAAT

501 TAAAGAGTAG GGTTTTTTTT CAGTATTCTT GGTTAATATT TAATTTCAAC TATTTATGAG ATGTATCTTT TGCTCTCTCT TGCTCTCTTA TTTGTACCGG

601 TTTTTGTATA TAAAATTCAT GTTTCCAATC TCTCTCTCCC TGATCGGTGA CAGTCACTAG CTTATCTTGA ACAGATATTT AATTTTGCTA ACACTCAGCT

701 CTGCCCTCCC CGATCCCCTG GCTCCCCAGC ACACATTCCT TTGAAATAAG GTTTCAATAT ACATCTACAT ACTATATATA TATATTTGGC AACTTGTATT

801 TGTGTGTATA TATATATATA TATGTTTATG TATATATGTG ATTCTGATAA AATAGACATT GCTATTCTGT TTTTTATATG TAAAAACAAA ACAAGAAAAA

901 ATAGAGAAAT CTACATACTA AATCTCTCTC CTTTTTTAAT TTTAATATTT GTTATCATTT ATTTATTGGT GCTACTGTTT ATCCGTAATA ATTGTGGGGA

1001 AAAGATATTA ACATCACGTC TTTGTCTCTA GTGCAGTTTT TCGAGATATT CCGTAGTACA TATTTATTTT TAAACAACGA CAAAGAAATA CAGACATAT

1101 G NdeI

Length: 1101 bp

FIGURE 15

VEGF 3'UTR hypoxia domain construct:

AUUUA {Bold/Underline}
Restriction Sites {Bold}

NotI

1 **GCGGCCGCAT** TCCTGTAGAC ACACCCACCC ACATACATAC **ATTTA**TATAT

51 ATATATATTA TATATATATA AAAATAAATA TCTCTATTTT ATATATATAA

101 AATATATATA TTCTTTTTTT AAATTAACAG TGCTAATGTT ATTGGTGTCT

151 TCACTGGATG **AACATATG**

NdeI

Length: 168 bp

FIGURE 16

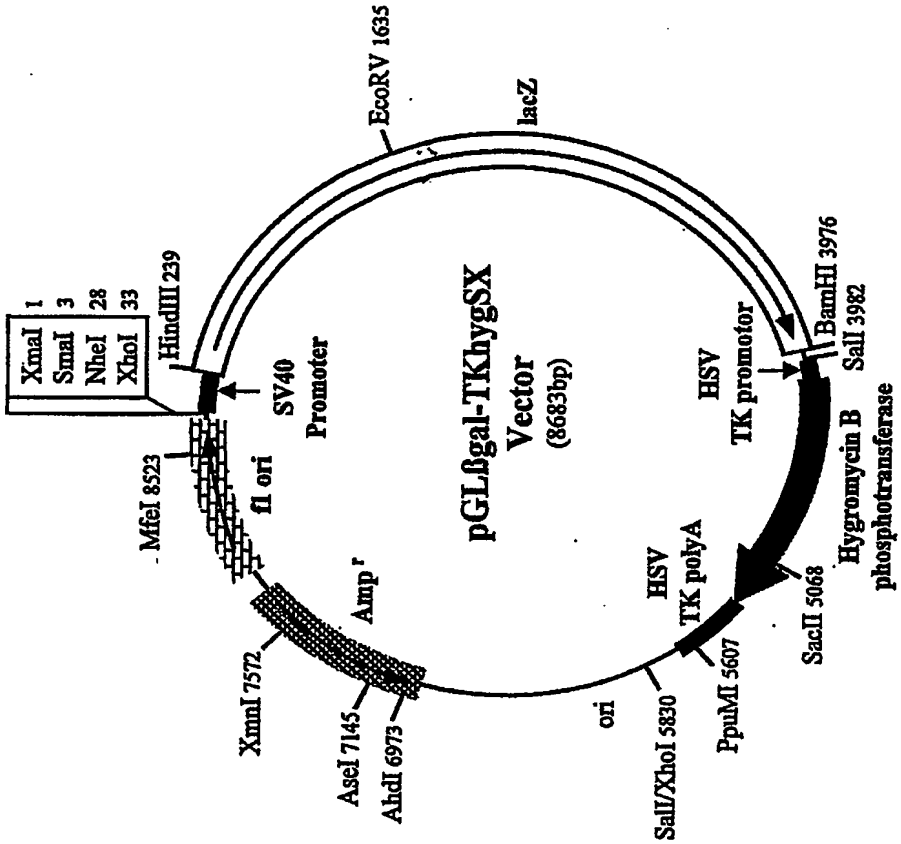
pGLßgal-TKhygSX
Vector
(8683bp)
XmaI 1
SmaI 3
NheI 28
XhoI 33
HindIII 239
EcoRV 1635
lacZ
BamHI 3976
SalI 3982
SV40
Promoter
HSV
TK promotor
Hygromycin B
phosphotransferase
SacII 5068
HSV
TK polyA
PpuMI 5607
SalI/XhoI 5830
ori
AhdI 6973
AseI 7145
XmnI 7572
Amp r
f1 ori
MfeI 8523

FIGURE 17